

Figure 1 (SEQ ID NO: 2878)

GATCAAACCTCTTTCCATTGAGAGTCCTCTGATTGAGATTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAAATTTCC
TTAATAAAAAATACAACTCAGATCCTTCAAATATGAACTGGTTGGGGAATCTCCATTTTTCAATATTATTTCTTCTTGTTTTTC
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAAC
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAA
AATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAACTATAACTTCCTCTTTAGAACTCCAACCACATTTGGATC

FIG. 2A (SEQ ID NOS: 2879 & 2880)

5' 9 18 27 36 45 54
CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
63 72 81 90 99 108
ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
117 126 135 144 153 162
TGG TCA CAG TTC AGC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
M M V D P N G N E S S
171 180 189 198 207 216
GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
A T Y F I L I G L P G L E E A Q F W
225 234 243 252 261 270
TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
L A F P L C S L Y L I A V L G N L T
279 288 297 306 315 324
ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
I I Y I V R T E H S L H E P M Y I F
333 342 351 360 369 378
CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
L C M L S G I D I L I S T S S M P K
387 396 405 414 423 432
ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
M L A I F W F N S T T I Q F D A C L
441 450 459 468 477 486
CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
L Q I F A I H S L S G M E S T V L L
495 504 513 522 531 540
GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
A M A F D R Y V A I C H P L R H A T
549 558 567 576 585 594
GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
V L T L P R V T K I G V A A V V R G
603 612 621 630 639 648
GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
A A L M A P L P V F I K Q L P F C R

FIG. 2B

657	666	675	684	693	702
TCC AAT ATC CTT TCC	CAT TCC TAC TGC CTA CAC	CAA GAT GTC ATG AAG CTG	GCC		
S N I L S H S Y C L H Q D V M K L A					
711	720	729	738	747	756
TGT GAT GAT ATC CGG	GTC AAT GTC GTC TAT GGC	CTT ATC GTC ATC ATC TCC	GCC		
C D D I R V N V V Y G L I V I I S A					
765	774	783	792	801	810
ATT GGC CTG GAC TCA CTT CTC ATC	TCC TTC TCA TAT CTG CTT ATT	CTT AAG ACT			
I G L D S L L I S F S Y L L I L K T					
819	828	837	846	855	864
GTG TTG GGC TTG ACA CGT GAA GCC	CAG GCC AAG GCA TTT GGC	ACT TGC GTC TCT			
V L G L T R E A Q A K A F G T C V S					
873	882	891	900	909	918
CAT GTG TGT GCT GTG TTC ATA TTC	TAT GTA CCT TTC ATT GGA TTG	TCC ATG GTG			
H V C A V F I F Y V P F I G L S M V					
927	936	945	954	963	972
CAT CGC TTT AGC AAG CGG CGT GAC	TCT CCG CTG CCC GTC ATC TTG	GCC AAT ATC			
H R F S K R R D S P L P V I L A N I					
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT CCT GTG CTC	AAC CCA ATT GTC TAT GGA GTG	AAG ACA AAG			
Y L L V P P V L N P I V Y G V K T K					
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC ATC CTT CGA	CTT TTC CAT GTG GCC ACA CAC	GCT TCA GAG			
E I R Q R I L R L F H V A T H A S E					
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG ATC AAA CTT	CTT TTC CAT TCA GAG TCC TCT	GAT TCA GAT			
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT TTG GAA GAC	AGT ATT CAG AAA AAA AAT TTC	CTT AAT AAA			
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT CCT TCA AAT	ATG AAA CTG GTT GGG GAA TCT	CCA TTT TTT			
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT CTT TGT TTT	CTT GCT ACA TAT AAT TAT TAA	TAC CCT GAC			
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA GGG TTA TTA	CTT TTC ATT TTA CCA TGC	AGT CCA AAT CTA			

FIG. 2C

1359	1368	1377	1386	1395	1404
AAC TGC TTC	TAC TGA TGG	TTT ACA GCA	TTC TGA GAT	AAG AAT GGT	ACA TCT AGA
1413	1422	1431	1440	1449	1458
GAA CAT TTG	CCA AAG GCC	TAA GCA CGG	CAA AGG AAA	ATA AAC ACA	GAA TAT AAT
1467	1476	1485	1494	1503	1512
AAA ATG AGA	TAA TCT AGC	TTA AAA CTA	TAA CTT CCT	CTT CAG AAC	TCC CAA CCA
1521	1530	1539	1548	1557	1566
CAT TGG ATC	TCA GAA AAA	TGC TGT CTT	CAA AAT GAC	TTC TAC AGA	GAA GAA ATA
1575	1584	1593	1602	1611	1620
ATT TTT CCT	CTG GAC ACT	AGC ACT TAA	GGG GAA GAT	TGG AAG TAA	AGC CTT GAA
1629	1638	1647	1656	1665	1674
AAG AGT ACA	TTT ACC TAC	GTT AAT GAA	AGT TGA CAC	ACT GTT CTG	AGA GTT TTC
1683	1692	1701	1710	1719	1728
ACA GCA TAT	GGA CCC TGT	TTT TCC TAT	TTA ATT TTC	TTA TCA ACC	CTT TAA TTA
1737	1746	1755	1764	1773	1782
GGC AAA GAT	ATT ATT AGT	ACC CTC ATT	GTA GCC ATG	GGA AAA TTG	ATG TTC AGT
1791	1800	1809	1818	1827	1836
GGG GAT CAG	TGA ATT AAA	TGG GGT CAT	ACA AGT ATA	AAA ATT AAA	AAA AAA AAA
1845	1854	1863	1872	1881	1890
GAC TTC ATG	CCC AAT CTC	ATA TGA TGT	GGA AGA ACT	GTT AGA GAG	ACC AAC AGG
1899	1908	1917	1926	1935	1944
GTA GTG GGT	TAG AGA TTT	CCA GAG TCT	TAC ATT TTC	TAG AGG AGG	TAT TTA ATT
1953	1962	1971	1980	1989	1998
TCT TCT CAC	TCA TCC AGT	GTT GTA TTT	AGG AAT TTC	CTG GCA ACA	GAA CTC ATG
2007	2016	2025	2034	2043	2052
GCT TTA ATC	CCA CTA GCT	ATT GCT TAT	TGT CCT GGT	CCA ATT GCC	AAT TAC CTG
2061	2070	2079	2088	2097	2106
TGT CTT GGA	AGA AGT GAT	TTC TAG GTT	CAC CAT TAT	GGA AGA TTC	TTA TTC AGA
2115	2124	2133	2142	2151	2160
AAG TCT GCA	TAG GGC TTA	TAG CAA GTT	ATT TAT TTT	TAA AAG TTC	CAT AGG TGA
2169	2178	2187	2196	2205	2214
TTC TGA TAG	GCA GTG AGG	TTA GGG AGC	CAC CAG TTA	TGA TGG GAA	GTA TGG AAT
2223	2232	2241	2250	2259	2268
GGC AGG TCT	TGA AGA TAA	CAT TGG CCT	TTT GAG TGT	GAC TCG TAG	CTG GAA AGT
2277	2286	2295	2304	2313	2322
GAG GGA ATC	TTC AGG ACC	ATG CTT TAT	TTG GGG CTT	TGT GCA GTA	TGG AAC AGG
2331	2340	2349	2358	2367	2376
GAC TTT GAG	ACC AGG AAA	GCA ATC TGA	CTT AGG CAT	GGG AAT CAG	GCA TTT TTG

FIG. 2D

2385	2394	2403	2412	2421	2430
CTT CTG AGG GGC	TAT TAC	CAA GGG TTA	ATA GGT TTC	ATC TTC AAC	AGG ATA TGA
2439	2448	2457	2466	2475	2484
CAA CAG TGT TAA	CCA AGA AAC	TCA AAT TAC	AAA TAC TAA	AAC ATG TGA	TCA TAT
2493	2502	2511	2520	2529	2538
ATG TGG TAA GTT	TCA TTT TCT	TTT TCA ATC	CTC AGG TTC	CCT GAT ATG	GAT TCC
2547	2556	2565	2574	2583	2592
TAT AAC ATG CTT	TCA TCC CCT	TTT GTA ATG	GAT ATC ATA	TTT GGA AAT	GCC TAT
2601	2610	2619	2628	2637	2646
TTA ATA CTT GTA	TTT GCT GCT	GGA CTG TAA	GCC CAT GAG	GGC ACT GTT	TAT TAT
2655	2664	2673	2682	2691	2700
TGA ATG TCA TCT	CTG TTC ATC	ATT GAC TGC	TCT TTG CTC	ATC ATT GAA	TCC CCC
2709	2718	2727	2736	2745	2754
AGC AAA GTG CCT	AGA ACA TAA	TAG TGC TTA	TGC TTG ACA	CCG GTT ATT	TTT CAT
2763	2772	2781	2790	2799	2808
CAA ACC TGA TTC	CTT CTG TCC	TGA ACA CAT	AGC CAG GCA	ATT TTC CAG	CCT TCT
2817	2826	2835	2844	2853	2862
TTG AGT TGG GTA	TTA TTA AAT	TCT GGC CAT	TAC TTC CAA	TGT GAG TGG	AAG TGA
2871	2880	2889	2898	2907	2916
CAT GTG CAA TTT	CTA TAC CTG	GCT CAT AAA	ACC CTC CCA	TGT GCA GCC	TTT CAT
2925	2934	2943	2952	2961	2970
GTT GAC ATT AAA	TGT GAC TTG	GGA AGC TAT	GTG TTA CAC	AGA GTA AAT	CAC CAG
2979	2988	2997	3006	3015	3024
AAG CCT GGA TTT	CTG AAA AAA	CTG TGC AGA	GCC AAA CCT	CTG TCA TTT	GCA ACT
3033	3042	3051	3060	3069	3078
CCC ACT TGT ATT	TGT ACG AGG	CAG TTG GAT	AAG TGA AAA	ATA AAG TAC	TAT TGT
3087	3096	3105	3114	3123	3132
GTC AAG AAA AAA	AAA AAA AAA	AAA AAA AAA	AAA AAA AAA	AAA AAA AAA	AAA AAA AAA

AAA A 3'

Figure 3: Protein Sequence for 101P3A11. (*piece of SEQ ID NO: 2880*)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTITYIVRTEHSLHEPMYIFLCMLSGIDILI
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRTKIGV
AAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL
LILKTVLGLTREAAKAFGTCVSHVCAVFIFYVPFIGLSMVHFRFSKRDSPLPVILANIYLLVPPVLNPVYG
VKTKEIRQRILRLFHVATHASEP

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

Query: 34 GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLFL 93
 GN + T FIL+GL L +Y + ++GNL II ++RT LH PMY+FL
 Sbjct: 6 GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94 SHLAFLDIGYSSSVTPIMLRGFLRKGTFFIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
 L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY
 Sbjct: 66 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGWVNAWIFTGCSLNL SFCGPNKINHFFCDYSP 213
 VAIC PL ++T ++ + + + G L FC N ++H +C +
 Sbjct: 126 VAICHPLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISSGSIIVTVFIIALSIVYILVSILKMRSTEGRQKAFSTCTS 273
 ++KL+C V I S I + +I+ SY+ IL ++L + + E + KAF TC S
 Sbjct: 186 VMKLACDDIRVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK---VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
 H+ AV +F+ + FI + +S ++ +++ Y +V P+LNP++Y + KE+++
 Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQ 302

Query: 330 AMKKL 334 (SEQ ID NO: 2881)
 + +L
 Sbjct: 303 RILRL 307 (SEQ ID NO: 2882)

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
 F+LIG+PGLEEA FW FPL S+Y +A+ GN +++IVRTE SLH PMY+FLCML+ ID+
 RA1C: 11 FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAIDL 70

PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
 +STS+MPK+LA+FWF+S I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
 RA1C: 71 ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCIHQDVMKLACDD 193
 HA VL +IG+ A+VRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
 RA1C: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLIIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
 NVVYGL I+ +G+D + IS SY LI++ VL L ++ +AKAFGTCVSH+ V F
 RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRDRSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQRILRLFHVA 311 (SEQ ID NO: 2223)
 YVP IGLS+VHRF D + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
 RA1C: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO: 2224)

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
 F+LIG+PGLE+A FW+ FPL S+Y++A+ GN +++IVRTE SLH PMY+FLCML+ ID+

GPCR: 11 FVLIGIPGLEKAHFWVGFPLLSMYVVMFGNCIVVFIVRTERS LHAPMYLFLCMLAIDL 70

PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
 +STS+MPK+LA+FWF+S I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR

GPCR: 71 ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
 HA VL +IG+ AVVRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D

GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194 IRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
 NVVYGL I+ +G+D + IS SY LI++TVL L ++ +AKAFGTCVSH+ V F

GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRILRLFHVA 311 (SEQ ID NO: 2885)
 YVP IGLS+VHRF + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++

GPCR: 251 YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPVINPIIYGAKTKQIRTVLAMFKIS 309 (SEQ ID NO: 2886)

Figure 25: Alignment with human olfactory receptor 5II12 (gi|14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66
 N + +F+L G+PGLE + WL+ PLC +Y +A+ GN I+ VR E SLHEPMY FL
 HOR5: 5 NVTHPAFFLLTGIPGLESSHWSLGLCVMYAVALGGNTVILQAVRVEPSLHEPMYFLS 64

PHOR: 67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
 MLS D+ IS +++P +L F N+ I FDACL+Q+F IH S MES +LLAM+FDYV
 HOR5: 65 MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
 AIC PLR+ATVLT + +G+ A R + PLP IK+LP CRSN+LSHSYCLH D+
 HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
 M+LAC DI +N +YGL V++S G+D I SY+LIL++V+ +RE + KA TCVSH
 HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFGLSMVHRFSKRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRIL 305
 + AV FYVP IG+S VHRF K + V+++N+YL VPPVLNP++Y KTKEIR+ I
 HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLMNSVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309 (SEQ ID NO: 2887)
 R+FH
 HOR5: 305 RMFH 308 (SEQ ID NO: 2888)